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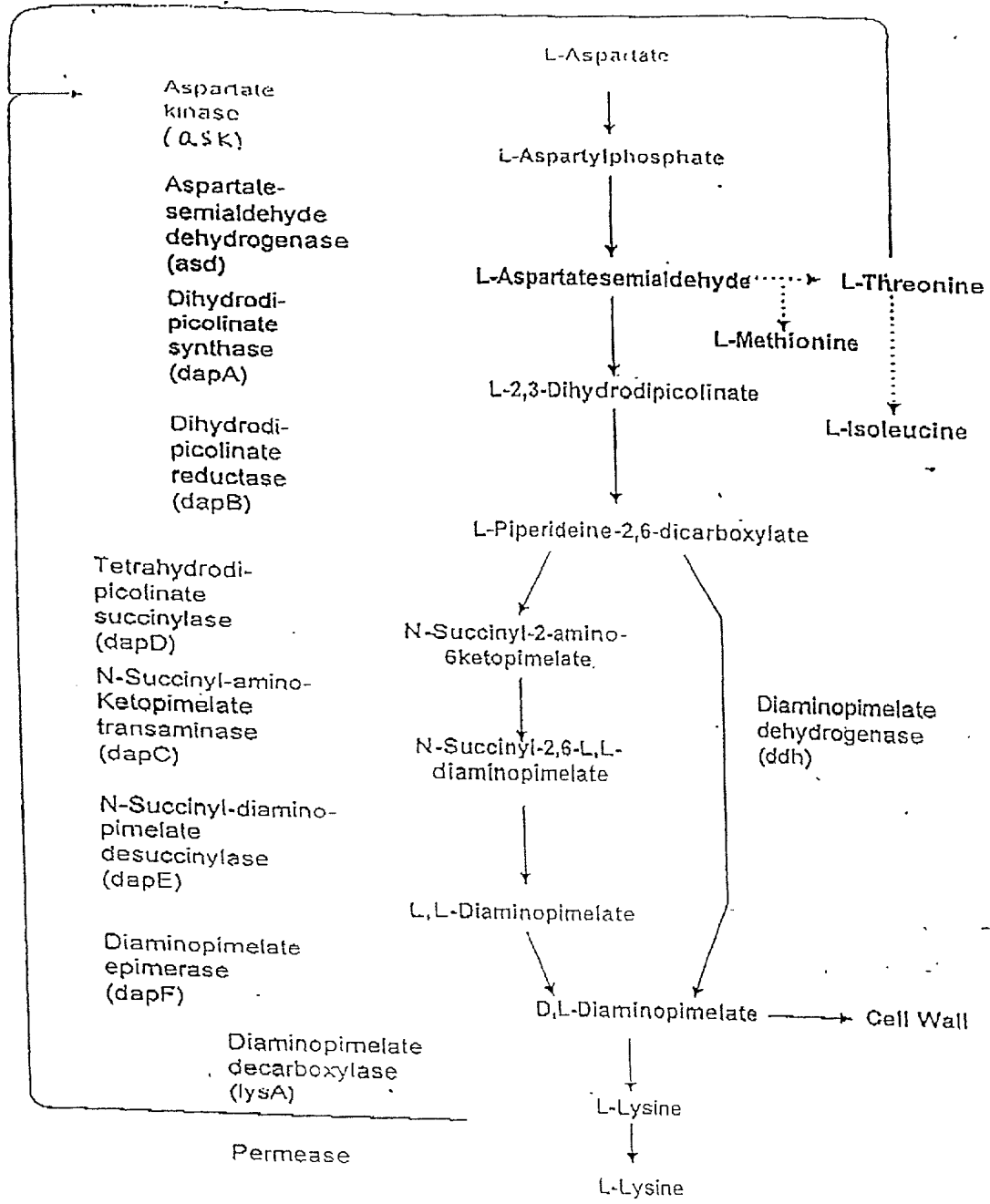


Fig 1

SEQ ID NO:1

Pro amino acid sequence of ATCC 71529 ant.

SEQ ID NO:2

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GTGGCCCTGGTCGTACAGAAATATGGCGTTCTCGCTTGACAGTGGCGAAGCAATTAGA
1 -----+-----+-----+-----+-----+ 60
P A L V V O K Y G G S S L E S A L P I R
AACGTGCTGAACGGATCGTTGCCACCAAGAGGCTCGAAA1GATGTCGTGGTCTCTGC
61 -----+-----+-----+-----+-----+ 120
N V A E R I V A T K K A G N O V V V V C
TCCGCAATGGGAGACACCACGGATGAACCTTCTAGAACTTGCAGCGGCAGTGAATCCCGTT
121 -----+-----+-----+-----+-----+ 180
S A M G D T T D E L L E L A A A V N P V
CCGCCAGCTCGTGAATGGATATGCTCCTGACTGCTGGTGAGCGTATTTCTAACGCTCTC
181 -----+-----+-----+-----+-----+ 240
P P A R E M D M L L T A G E R I S N A L
GTGCCCATGGCTATTGAGTCCCTTGGCGCAGAAGCTCAATCTTCACTGGCTCTCAGGCT
241 -----+-----+-----+-----+-----+ 300
V A M A I E S L G A E A Q S F T G S Q A
GGTGTGCTCACCACCGAGCGCCACGGAACGCACGCATTGTTGACGTACACCGGGTCTG
301 -----+-----+-----+-----+-----+ 360
G V L T T E R H G N A R I V D V T P G R
GTGCGTGAAGCACTCGATGAGGGCAAGATCTGCATTGTTGCTGGTTTTTCAGGGTGTAAAT
361 -----+-----+-----+-----+-----+ 420
V R E A L D E G K I C I V A G F Q G V N
AAAGAAACCCCGCATGTACCAACGTTGGGTGCTGGTGGTTCTGACACCACTGCAGTTGCG
421 -----+-----+-----+-----+-----+ 480
K E T R D V T T L G R G G S D T T A V A
TTGGCAGCTGCTTGAACGCTGATGTGTGTGAGATTTACTCGACGTTGACGGTGTGTAT
481 -----+-----+-----+-----+-----+ 540
L A A A L N A D V C E I Y S D V D G V Y
ACCGCTGACCCGCGCATCGTTCTAATGCACAGAAGCTGGAAAGCTCAGCTTCGAAGAA
541 -----+-----+-----+-----+-----+ 600
T A D P R I V P N A Q K L E K L S F E E
ATGCTGGAACCTTGCTGCTGTTGGCTCCAAGATTTTGGTGTGCGCAGTGTGAATACGCT
601 -----+-----+-----+-----+-----+ 660
M L E L A A V G S K I L V L R S V E Y A
CGTGCATTCAATGTGCCACTTCGCGTACGCTCGTCTTATAGTAATGATCCCGGCACCTTG
661 -----+-----+-----+-----+-----+ 720
R A F N V P L R V R S S Y S N D P G T L
ATTGCCGGCTCTATGGAGGATATTCCTGTGGAAGAAGCAGTCCTTACCGGTGTCCGAACC
721 -----+-----+-----+-----+-----+ 780
I A G S M E D I P V E E A V L T G V A T
GACAAGTCCGAAGCCAAAGTAACCGTTCTGGGTATTTCCGATAAGCCAGCGCAGGCTGCC
781 -----+-----+-----+-----+-----+ 840
D K S E A K V T V L G I S D K P G E A A
```

Fig 2A

30x
114

SEQ ID NO:1
(Cont)

1841 AAGGTTTTCCTGCGTTGGCTGATGCAGAAATCAATATTGACATGGTTCTCAGAACGTC 900

SEQ ID NO:2
(Cont)

K V F R A L A D A E I E I D K V L D N Y

901 TCCTCTGTGGAAGACGGCACCACCGACATCAGTTTACCTGCCCTCGGGCTGACGGACGGC 960

S S V E D G T T D E T F T C P R A D G R

961 CGTGCGATGGAGATCTTGAAGAAGCTTCAGGTTCAAGGCAACTGGACCAATGTGCTTTAC 1020

R A M E I L K K L Q V Q G N W T N V L Y

1021 GACGACCAGGTCGGCAAAGTCTCCCTCGTGGGTGCTGGCATGAAGTCTCACCAGGTGTT 1080

D D Q V G K V S L V G A G M K S H P G V

1081 ACCGCAGAGTTCATGGAAGCTCTGCGCGATGTCAACSTGAACATCGAATTGATTTCCATC 1140

T A E F M E A L R E V N V N I E L I S I

1141 TCTGAGATCCGCATTTCCGTGCTGATCCCTGAAGATGATCTGGATGCTGCTCAGGTGCA 1200

S E I R I S V L I R E D D L D A A A K A

1201 TTGCATGAGCAGTTCCAGCTGGGCGGCGAAGACGAAGCCGTCGTTTATGCAGGCACCGGA 1260

L H E Q F Q L G G E D E A V V Y A T T G

CGCTAA
1261 ----- 1266

R *

Fig 2B

SEQ ID NO: 3
SEQ ID NO: 4

Fig 3A

0:3 TCCCTCGTTGGACGCATCCGTCAGGACTCCACTGTGCGACGACAACCGCGGTCTCGTTCTC
901 ----- 960

[illegible]

V V S G D N L R K G A A L N T I Q I A E

CTGCTGGTTAAGTAA

1021 -----+----- 1035

L L V K "

Fig 3B

Amino acid sequence of dapB

SEQ ID NO: 5 ATGGGAATCAAGGTTGGCGTTCTCGGAGCCAAAGGCCGTGTTGGTCAAACCTATTGTGGCA
1 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 60

SEQ ID NO: 6 M G I K V G V L G A K G R V G Q T I V A
GCAGTCAATGAGTCCGACGATCTGGAGCTTGTTCAGAGATCGGCGTCGACGATGATTG
61 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 120
A V N E S D D L E L V A E I G V D D D L
AGCCTTCTGGTAGACAACGGCGCTGAAGTTGTCTGTTGACTTCACCACTCCTAACGCTGTG
121 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 180
S L L V D N G A E V V V D E T T P N A V
ATGGGCAACCTGGAGTTCTGCATCAACAACGGCATTCTGCGGTTGTTGGAACACGGGC
181 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 240
M G N L E F C I N N G I S A V V G T T G
TTCGATaATGCTCGTTTGGAGCAGGTTCTCGGCTGAGGCTGAAGGAAAAGACAATGTCGGT
241 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 300
F D N A R L E Q V R A W L E G K D N V G
GTTCTGATCGCACCTAACTTTGCTATCTCTGCGGTGTGACCATGGTCTTTTCCAAGCAG
301 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 360
V L I A P N F A I S A V L T M V F S K Q
GCTGCCCGCTTCTTCAATCAGCTGAAGTTATTGAGCTGCACCACCCCAACAAGCTGGAT
361 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 420
A A R F F E S A E V I E L H H P N K L D
GCACCTTCAGGCACCGCGATCCACACTGCTCAGGGCATTGCTGCGGCACGCAAAGAAGCA
421 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 480
A P S G T A I H T A Q G I A A A R K E A
GGCATGGACGCACAGCCAGATGCGACCGAGCAGGCACTTGAGGCTTCCCGTGGCGCAAGC
481 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 540
G M D A Q P D A T E Q A L E G S R G A S
GTAGATGGAATCCCaGTTCAcGCAGTCCGCATGTCCGGCATGGTTGCTCAGAGCAAGTT
541 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 600
V D G I P V H A V R M S G M V A H E Q V
ATCTTTGGCACCCAGGTCAGACCTTGACCATCAAGCAGGACTCCTATGATCGCAACTCA
601 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 660
I F G T Q G Q T L T I K Q D S Y D R N S
TTTGACCCAGGTGTCTTGGTGGGTGTGCGCAACATTGCACAGCACCCAGGCCTAGTCGTA
661 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 720
F A P G V L V G V R N I A Q H P G L V V
GGACTTGAGCAATTACCTAGGCCTGTAA
721 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 747
G L E H Y L G L +

Fig 4

SEQ ID NO: amino acid sequence of ddh.

SEQ ID NO: 7

SEQ ID NO: 8

```
ATGTTATTTGGTAACTCGACCGGCTGTCGCGGCTGTTATTTGGGAGATTACAGAGAC
60
H F F G F L D Q D S A T T I L E D Y K N
ATGAGCAACATCGGGTAGCTATCGTGGCTACCGAAAGCTGGGACCGAGCGTCGMAAAG
120
H T N I F V A I V G Y C H L G R S V E K
CTTATTGCCAAGCAGCGCGACATGGACCTTGTAGGAATCTTCTCGCGCGCGCGCCACCGTC
180
L I A K Q P D H D L V G I F S R R K T L
GACACAAAGACCGCAGTCTTTGATGTCGCGGACGTGGACAAGCAGCGCGAGCGAGTGGAG
240
D T K T P V E D V A D V D K H A O D V D
GTGCTGTTCTGTGCTGGGCTCGCGCAGCGAGATCGCTGAGCAGGCAACCAGGTTCCGGC
300
V L F L C H G S A T D I P C Q A P K F A
CAGTTCGCGCTGCACCGTAGACACCTACGACAACCGCGGACATCCGACGCGCAGCGCGAG
360
O F A C T V D T Y D N H R D I P R R Q
GTGAGAAAGCAAGCGCGCAGCGCGGCAAGCTTGCACTGGTCTGTACCGGCTGGGAT
420
V M N E A A T A A C N V A L V S T S W D
CGAGGAATGTTCTCCATCAACCGCGTGTACGCGAGCGCGGACTGTTAGCGGAGCAGCAGCAG
480
P G H F S I N R V Y A A A V L A E H O Q
CAGACCTTCTGGGCGCGAGCTTGTGACAGGGCGCACTCCGATGCTTGGCAAGCATCCCT
540
H T F H G P G L S Q G H S D A L R P I P
GGCGTCAAAAGCGCGTCCAGTACCGCTCCCATCCCAAGAGCGCGTGGCAAGAGCGCGCG
600
G T Q K A V Q Y T L P S E E A L E H A R
CGTGGGAAAGCGCGGACCTCAGCGGAAAGCAAAACCAAGCGCGCAATGCTTCGTGGTT
660
R G E A G D L T G K Q T H R O C F V V
CGCGAGCGCGCGGAGCAGGAGCGCATCGAANAGGACATCCGACCATCGCTGATTACTTC
720
A D A A D H E R I E N D I R T H E D Y F
GTTGGCTACGAAGTCGAAGTCAACTTCAGGAGCAAGCAACCTTGACGCGCGAGCACACCC
780
V G Y E V E V N F I D E A T L D A E H T
GGCATGCCACAGCGGAGGACAGGTGATCACCACCGCGGACACCGGTGCTTAAAGCAGACC
840
G K P H G G H V I T T C D T G C F N H T
GTGGGATACATCTGAAAGCTGGACCGAAGCCAGATTTACCGGCTTCTTACAGATCCCT
900
V E Y I L K L D R N P O E T A S S Q I A
TTGGGCTGGCGAGCTCAGCGCATGAAGCAGCAGGCGCAAGCGGTGCTTTACCGTGGTC
```

Fig 5A

901 ----- 900

Г Г Р А А И Р М К О О Г О С Г А Ф Т О Л

SEQ ID NO: 7
(Cont)

GAAGTTGCTCCATACtTGCTCTCCCCgGAACCTTGGtGATCTGATCGCACTCGAAGTTC

[illegible]

SEQ ID No. 8
(cont)

E V A P Y L L S P E N L D D L I A P D V

TAA

1021 --- 1023

Fig 5B

ORF2 amino acid sequence

1 ----- 60

M A E O V K L S V E L I A C S S F T E P

[illegible]

CGTGCCTGCTACGAAACTTTTGATAAGCCGAACCTCGAACTGCTTCCAATGCTGCGTAT
121 -----+-----+-----+-----+-----+-----+-----+ 180

CTGCGCCACATCATGGAAGTGGGGCACACTGCTTTGCTTGAGCÂTGCCAAATGCCACGATG
181 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 240

241 TATATCCGAGGCATTTCTCGGTCCGCGACCCATGAATTGGTCCGACCCGCCATTTTCC 300

301 TTCTCTCAACTGTCTCAGCGTTTCGTGCACAGCGGAGAATCGGAAGTAGTGGTGCCCACT 360

CTCATCGATGAAGATCCGCAGTTGCGTGAACCTTTTCATGCACGCCATGGATGAGTCTCGG
361 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 420

421 TTCGCTTTCAATGAGCTGCTTAATGCGCTGGAAGAAAACTTGGCGATGAACCGAATGCA 480

CTTTTAAGGAAAAAGCAGGCTCGTCAAGCAGCTCGCGCTGTGCTGCCCAACGCTACAGAG
481 -----+-----+-----+-----+-----+-----+-----+ 540

541 TCCAGAATCGTGGTGTCTGGAACTTCCGCACCTGGAGGCATTTCATTGGCATGCGAGCC 600

AGTGAACATGCAGACGTCGAAATCCGCGAAGTAGCGGTAGGATGTTTAAGAAAGCTGCAG
601 -----+-----+-----+-----+-----+-----+-----+ 660

GTAGCAGCGCCAACTGTTTTCGGTGATTTTGAGATTGAAACTTTGGCAGACGGATCGCAA
661 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 720

ATGGCAACAAGCCCGTATGTCATGGACTTTTAA
721 -----+-----+-----+-----753

M A T S P Y V M D F *

Fig 6

Full length amino acid sequence of LysA (pRS4)

Seq ID No. 11

ATGGCTACAGTTGAAAAATTTCAATGAACITCCCGCACACGTATGGCCACGCCATGGCCGTG
-----+-----+ 60

Seq ID No. 12

M A T V E N F N E L P A H V W P R E A V
CGCCAAGAAGACGGCGTTGTACCGTCGCTGGTGTGCCCTCTGCCTGACCTCGCTGAAGAA
61 -----+-----+ 120
R Q E D G V V T V A G V P L P D L A E E
TACGGAACCCCACTGTTCTAGTCGACGAGGACGATTTCGGTTCCCGCTGTGCGGACATG
121 -----+-----+ 180
Y G T P L F V V D E D D F R S R C R D M
GCTACCGCATTCCGGTGGACCAAGCAATGTGCACTACGCATCTAAAGCGTTCCTGACCAAG
181 -----+-----+ 240
A T A F G G P G N V H Y A S K A F L T K
ACCATTGCACGTTGGGTTGTATGAAGAGGGGCTGGCACTGGACATTGCATCCATCAACGA
241 -----+-----+ 300
T I A R W V D E E G L A L D I A S I N E
CTGGGCATTGCCCTGGCCGCTGGTTTCCCCGCCAGCCGTATCACCGCGCACGGCAACAAC
301 -----+-----+ 360
L G I A L A A G F P A S R I T A H G N N
AAAGGCGTAGAGTTCTCTGCGCGCTTGTTTCAAACGGTGTGGGACACGTGGTGTCTGGGAC
361 -----+-----+ 420
K G V E F L R A L V Q N G V G H V V L D
TCCGCACAGGAAGTAGAAGTGTGGATTACGTTGCCGCTGGTGAAGGCAAGATTACAGGAC
421 -----+-----+ 480
S A Q E L E L L D Y V A A G E G K I Q D
GTGTTGATCCGCGTAAAGCCAGGCATCGAAGCACACACCCACGAGTTCATCGCCACTAGC
481 -----+-----+ 540
V L I R V K P G I E A H T H E F I A T S
CACGAAGACCAGAAGTTCGGATTCTCCCTGGCATCCGGTTCGCGATTGGAAGCAGCAAAA
541 -----+-----+ 600
H E D Q K F G F S L A S G S A F E A A K
GCCGCCAACAACGCAGAAAACTGAACCTGGTTGGCTGCACTGCCACGTGGTTCCCGAG
601 -----+-----+ 660
A A N N A E N L N L V G L H C H V G S Q

Fig 7A

Σ₁ ID No 12

F's 7B

Lys A (pRS6)

(Cont)

Seq ID 11

1321

CTCTCACTAGAGGCATAA

1338

Sq 10 No 12

L. S. L. E. A.

[illegible]

Fig 7C

Truncated ORF2
amino acid sequence

Seq ID No: 13

1 GTGGCCGAACAAGTTAAATTGAGCGTGGAGTTGATAGCGTGCAGTTCTTTTACTCCACCC
-----+-----+-----+-----+-----+ 60

Seq ID No: 14

M A E Q V K L S V E L I A C S S E T E P

61 GCTGATGTTGACTGGTCAACTGATGTTGAGGGCGCGGAGCACTCGTGCAGTTTCGGGGT
-----+-----+-----+-----+-----+ 120

A D V E W S T D V E G A E A L V E F A G

121 CGTGCCTGCTACGAAACTTTTGATAAGCCGAACCCCTCGAACTGCTTCCAATGCTGCGTAT
-----+-----+-----+-----+-----+ 180

R A C Y E T F D K P N P R T A S N A A Y

181 CTGCGCCACATCATGGAAGTGGGGCAGACTGCTTTGCTTGAGCATGCCAATGCCACGATG
-----+-----+-----+-----+-----+ 240

L R H I M E V G H T A L L E H A N A T M

241 TATATCCGAGGCATTTCTCGGTCCGCGACCCATGAATTGGTCCGACACCGCCATTTTTC
-----+-----+-----+-----+-----+ 300

Y I R G I S R S A T H E L V R H R H F S

301 TTCTCTCAACTGTCTCAGCGTTTCGTGCACAGCGGAGAATCGGAAGTAGTGGTGCCCACT
-----+-----+-----+-----+-----+ 360

F S Q L S Q R F V H S G E S E V V V P T

361 CTCAT ...

L (I)

Fig 8

Sequence encoded in the HpaI-PvuII fragment containing the P1

SEQ ID NO:15

AACCGGTGTGGAGCCGACCATTCCGCGAGGCTGCACTGCAACGAGGTGCTAGTTTTGGTACATGGCTTCTG
GCCAGTTCATGGATTGGCTGCCGAAGAAGCTATAGGCATCGCCACCAGGGCCACCGGAGTTACCGAAGAT
GGTGCCGTGCTTTTCGCCTTGGGCAGGGACCTTGACAAAGCCCACGCTGATATCGCCAAGTGAGGGATCAG
AATAGTGCATGGGCACGTCGATGCTGCCACATTGAGCGGAGGCAATATCTACCTGAGGTGGGCATTCTTCC
CAGCGGATGTTTTCTTGGCTGCTGCAGTGGGCATTGATACCAAAAAGGGGCTAAGCGCAGTCGAGGCGG
CAAGAACTGCTACTACCTTTTTTATTGTCGAACGGGGCATTACGGCTCCAAGGACGTTTGTTCCTGGGTCA
GTTACCCCAAAAAGCATATACAGAGACCAATGATTTTTCATTAAAAAGGCAGGGATTGTTATAAGTATGG
GTCGTATTCTGTGCGACGGGTGTACCTCGGCTAGAATTTCTCCCATGACACCAG

Figure 9

ATCC 13032	1		50
N13		V	
ATCC 21529		C	
Consensus		C	
		KALVVQKYGG SSLESAERIR NVAERIVATK KAGNDVWVC SAKGOTTDEL	
ATCC 13032	51		100
N13			
ATCC 21529			
Consensus		LELAHAVNPV PPAREMDMLL TAGERISNAL VAMATESLGA EAQSFTGSQA	
ATCC 13032	101		150
N13			
ATCC 21529			
Consensus		GVLTERHGN ARIVDVTGR VREALDEGKI CIVAGFQGVN KETRDVTTLG	
ATCC 13032	151		200
N13			
ATCC 21529			
Consensus		RGGSDTTAVA LAAALNAOVC EIYSOVGVY TADPRIVPNA QZLEKLSFEE	
ATCC 13032	201		250
N13			
ATCC 21529			
Consensus		MLELAAVGSK ILVLSVEYA RAFNVPLRV SSYSNDPGTL IAGSMEDIPV	
ATCC 13032	251		300
N13			
ATCC 21529			
Consensus		EEAVLTGVAT DKSEAKVTVL GISDKPGEAA KVFRALADAE IKIDMVLQNV	
ATCC 13032	301		350
N13		S	G
ATCC 21529		A	D
Consensus		A	G
		SSVEDGTTDI TPTCPRADGR RAKELUKKLQ VEGNWTNVLV DTQVGHVSLV	
ATCC 13032	351		400
N13		T	
ATCC 21529		T	
Consensus		I	
		GAGMKSHPGV TAEFMEALRD VNVNIELIST SEIRISVLIR EDDLDAARA	
ATCC 13032	401	421	
N13			
ATCC 21529			
Consensus		LHEQFQLGGE DEAVVYACTG R	

Fig 10

fig 11a

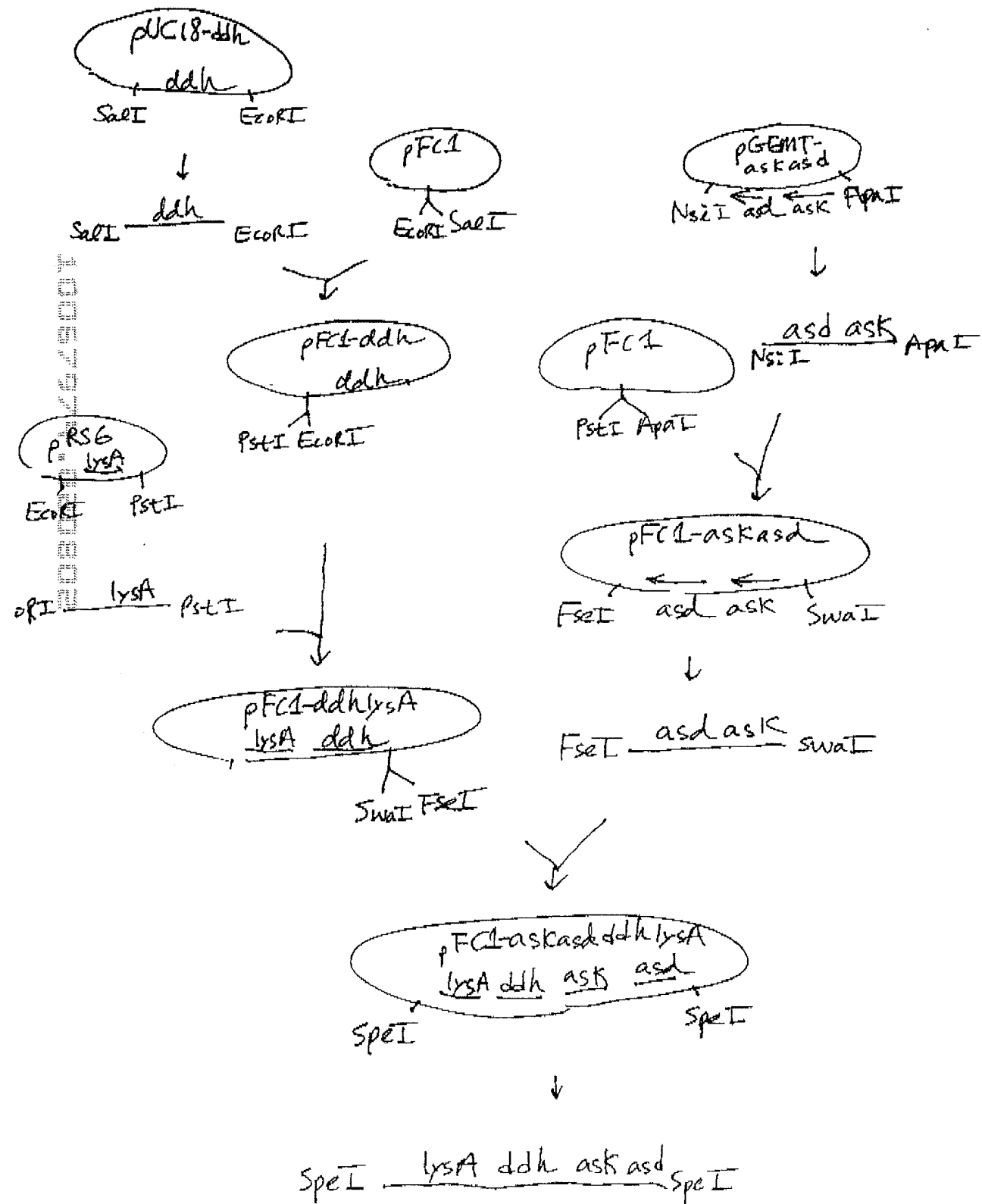
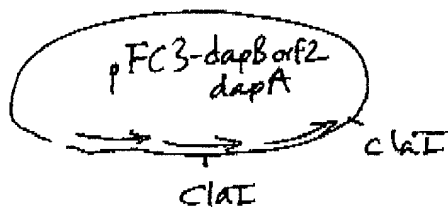
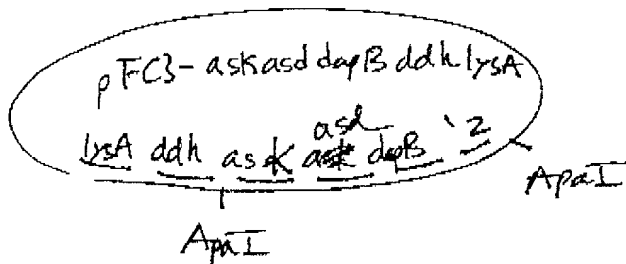
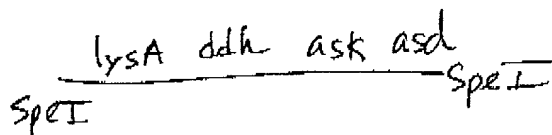
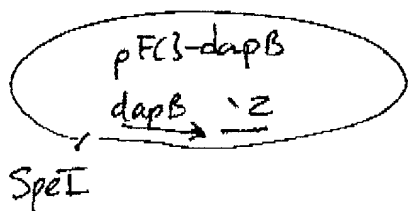


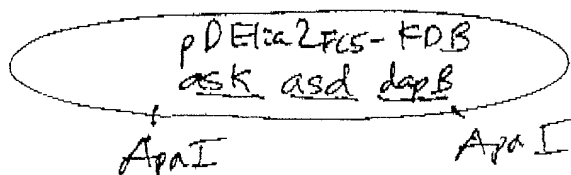
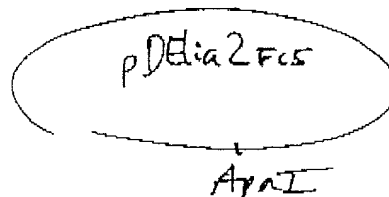
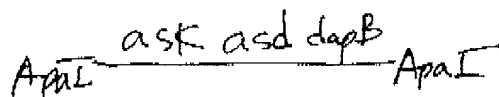
Fig 11 b



↓



↓



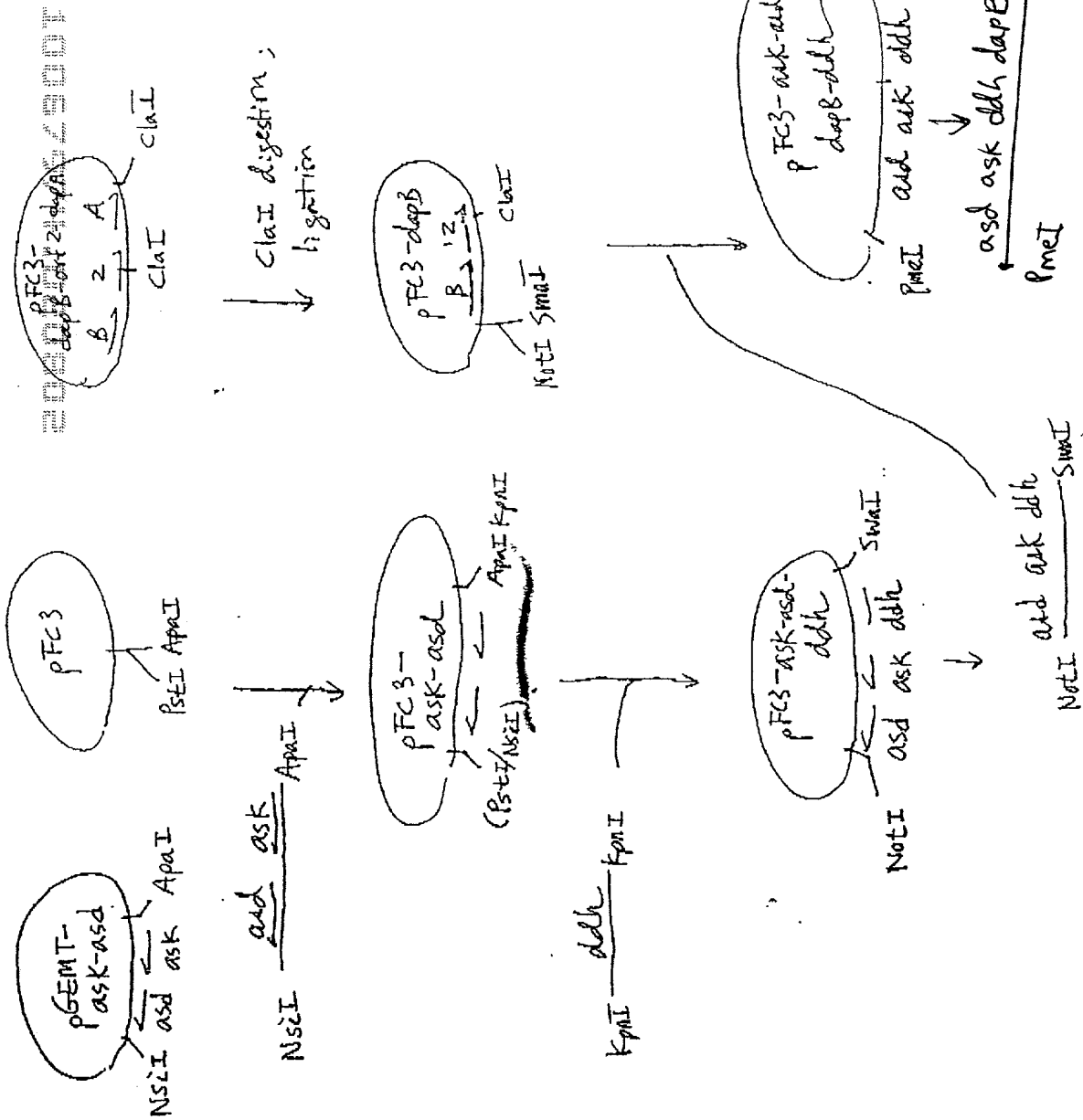


Fig 12

pDELia2FCS - ask asd dapB orf2 (pDELia2FCS - KDBZ)

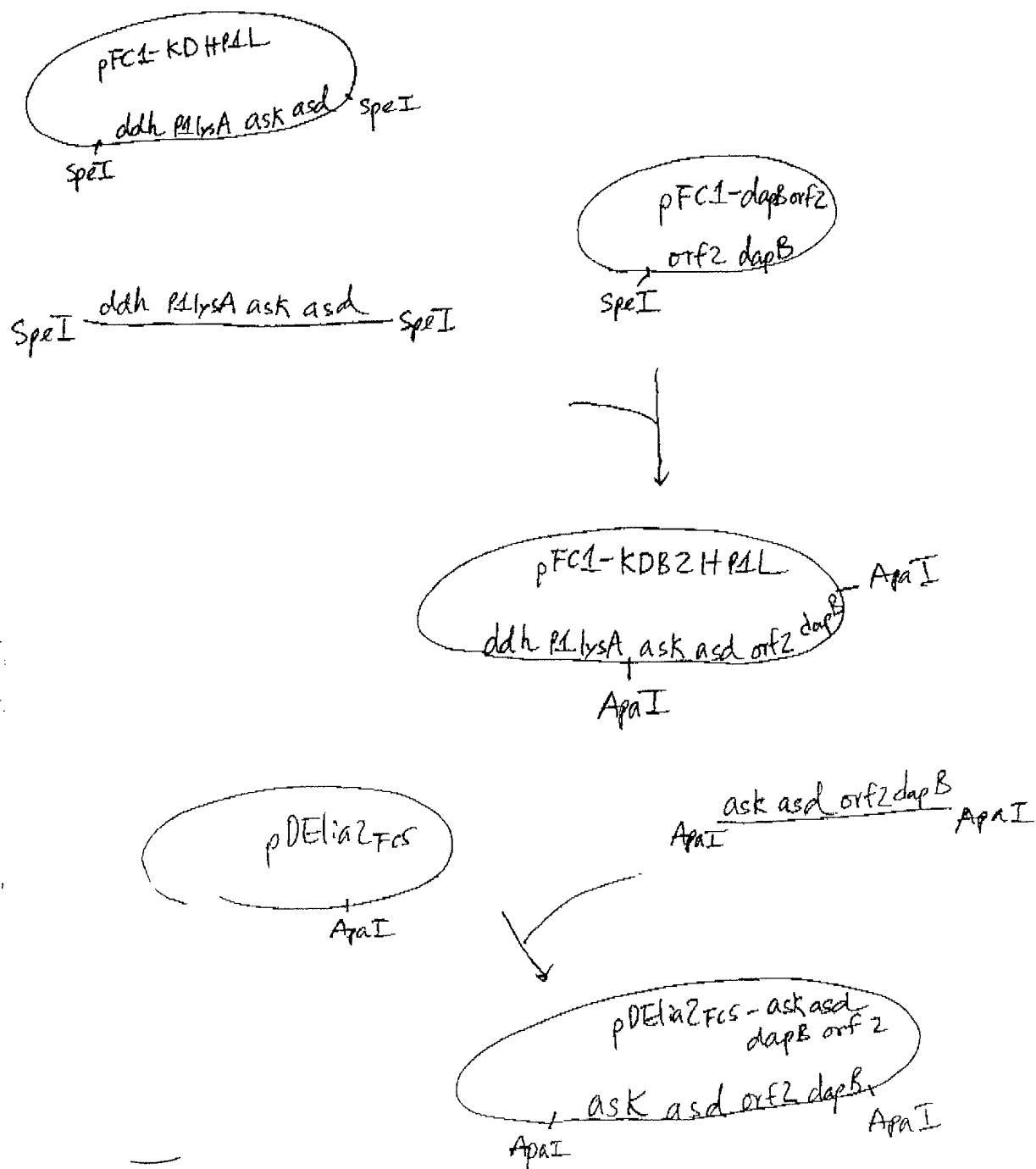


Fig 13

pDELia 2 FCS - ask asd ~~dapB~~ orf2 ddh pLysA

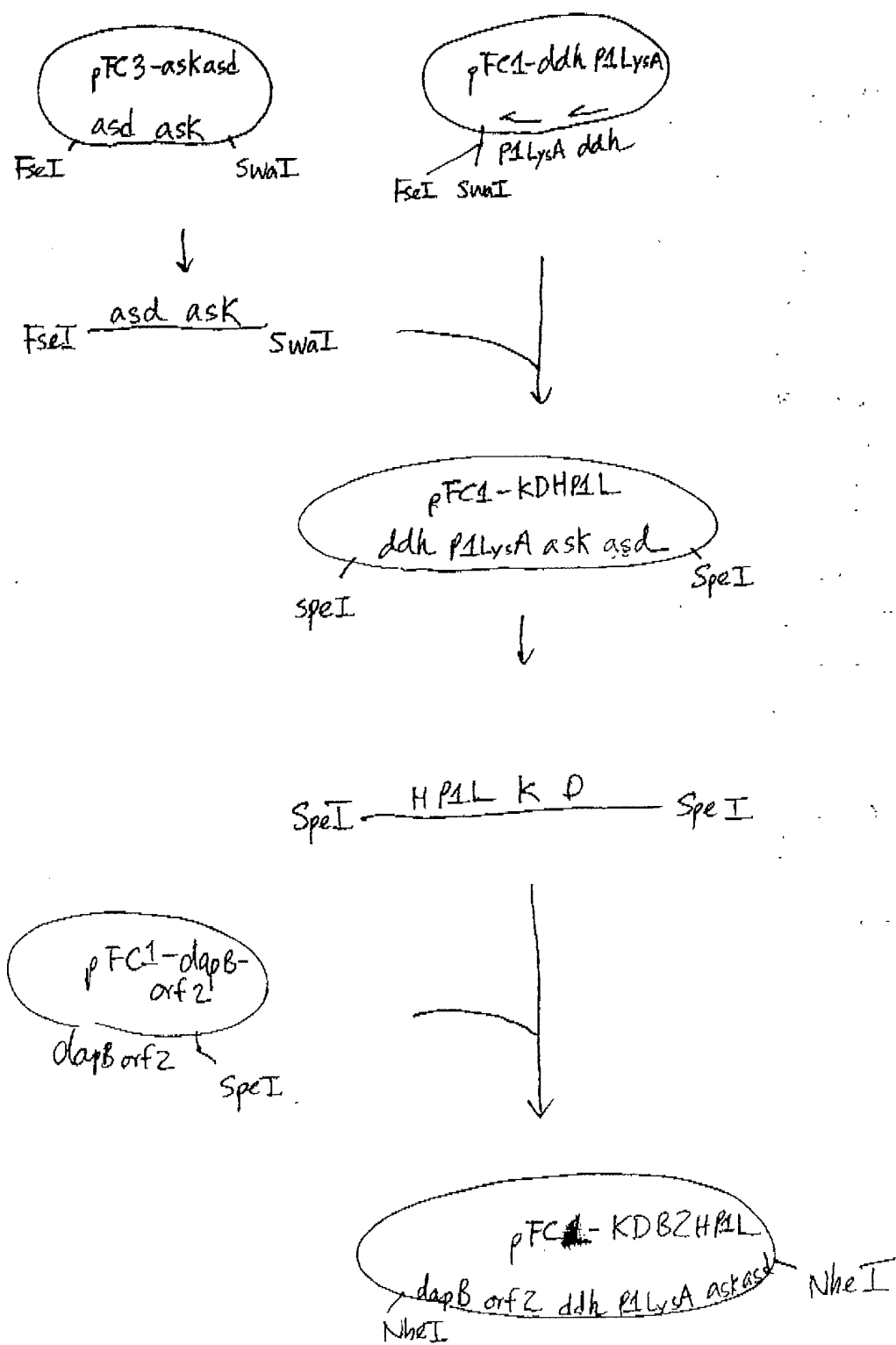


Fig. 24A

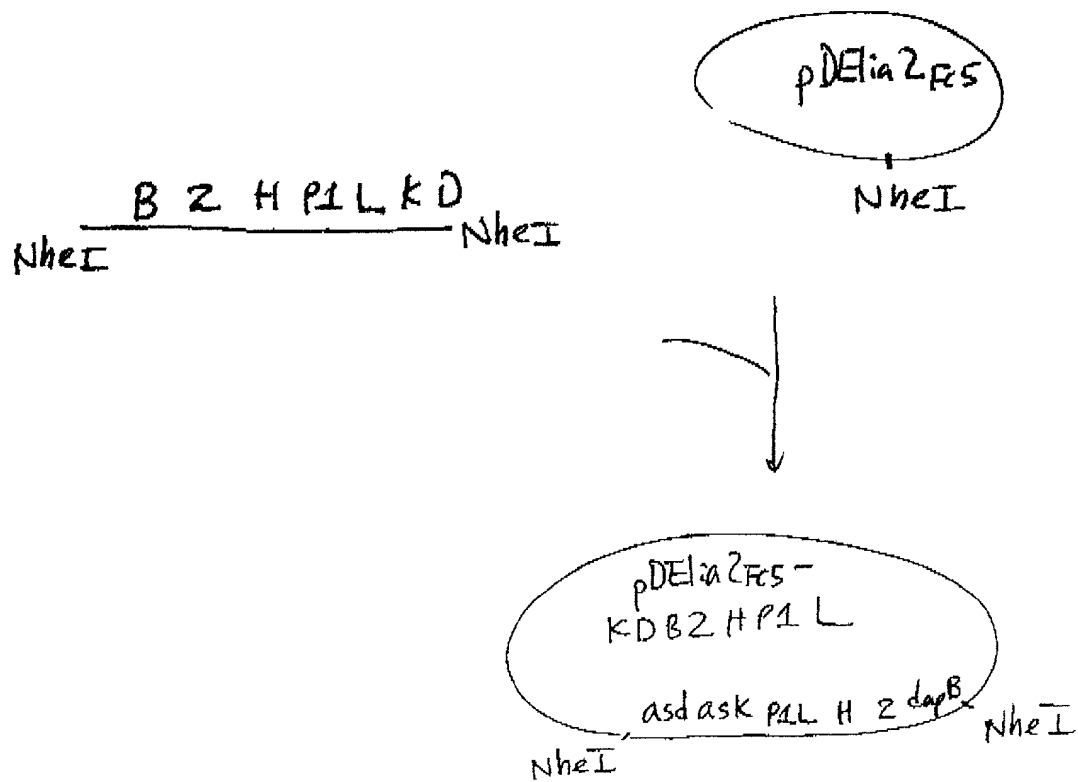


Fig. 14B